

SEQ ID NO.1FIG.1 a

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(UPPER:SEQ ID NO.1)
	19(LOWER:SEQ ID NO.1)
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119
	39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGAACAAG	239
	79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATAACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
TTGATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAGG	419
F I F G F V G N M L V I L I L I N C K R	139
CTCAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539
L T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
C T Q L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAATCGATAGGTACCTGGCTGTGCTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACA	
H F P Y	

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(UPPER:SEQ 1) NO.2
	19(LOWER:SEQ 1) NO.5
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119
	39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTTATTTATGCACAGGGTGGAACAAG	239
	79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
K I N V K Q I A A R L L P P L Y S L V	119
TCATCTTTGGTTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
I F G F V G N M L V I L I L I N C K R	139
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539
T V P F W A H Y A A A Q W D F G N T M	179
TTTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
Q L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC	839
H F P Y S Q Y Q F W K N F Q T L K I V I	279

TTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACT	899
L G L V L P L L V M V I C Y S G I L K T	299
CTGCTTCGGTGTGCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC	959
L L R C R N E K K R H R A V R L I F T I	319
ATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC	1019
M I V Y F L F W A P Y N I V L L L N T F	339
CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG	1079
Q E F F G L N N C S S S N R L D Q A M Q	359
GTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTC	1139
V T E T L G M T H C C I N P I I Y A F V	379
GGGGAGAAGTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC	1199
G E K F R N Y L L V F F Q K H I A K R F	399
TGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC	1259
C K C C S I F Q Q E A P E R A S S V Y T	419
CGATCCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT	1319
R S T G E Q E I S V G L *	439
GAGCCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACAGCCTGGGCTGGGGGTNGG	1379
	459
TTGGNNGAGGTCTTTTTTAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT	1439
	479
TATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC	

SEQ ID NO.2 (SUITE)

FIG.1c

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC 59(UPPER:SEQ ID NO.3
19(LOWER:SEQ ID NO.4

TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT 119
39

CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTTCATGGAGGGCAAC 179
59

TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTTATTTATGCACAGGGTGGAACAAG 239
79

ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299
M D Y Q V S S P I Y D I N Y Y T S E P C 99

CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359
K I N V K Q I A A R L L P P L Y S L V 119

TTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCACTCCTCATCCTGATAAACTGCAAAGG 419
I F G F V G N M L V I L I L I N C K R 139

CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479
K S M T D I Y L L N L A I S D L F F L 159

CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG 539
T V P F W A H Y A A A Q W D F G N T M 179

TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC 599
Q L L T G L Y F I G F F S G I F F I I 199

CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG 659
L L T I D R Y L A V V H A V F A L K A R 219

ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT 719
T V T F G V V T S V I T W V V A V F A S 239

CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT 779
L P G I I F T R S Q K E G L H Y T C S S 259

CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCCTGCCGCTGCTTGTTCATGGT 839
H F P Y I K D S H L G A G P A A A C H G 279

SEQ ID NO.3FIG.1d

CATCTGCTACTCGGGAATCCTAAAACTCTGCTTCGGTGTGCGAAATGAGAAGAAGAGGCA	899
H L L L G N P K N S A S V S K *	299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA	959
	319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019
	339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079
	359
CATCAACCCCATCATCTATGCCTTTGTGCGGGGAGAAGTTCAGAACTACCTCTTAGTCTT	1139
	379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199
	399
TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259
	419
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319
	439
TTGATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT	1379
	459
GTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC	1439
	479
GAATTC	

SEQ ID NO.3 (SUITE)

FIG.1e

FIG. 2

CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4	I		II	
	1	1	1	1
	1	1	1	1
	1	1	1	1
	1	1	1	1
CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4	II		III	
	1	1	1	1
	1	1	1	1
	1	1	1	1
	1	1	1	1
CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4	IV		V	
	1	1	1	1
	1	1	1	1
	1	1	1	1
	1	1	1	1
CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4	VI		VII	
	1	1	1	1
	1	1	1	1
	1	1	1	1
	1	1	1	1

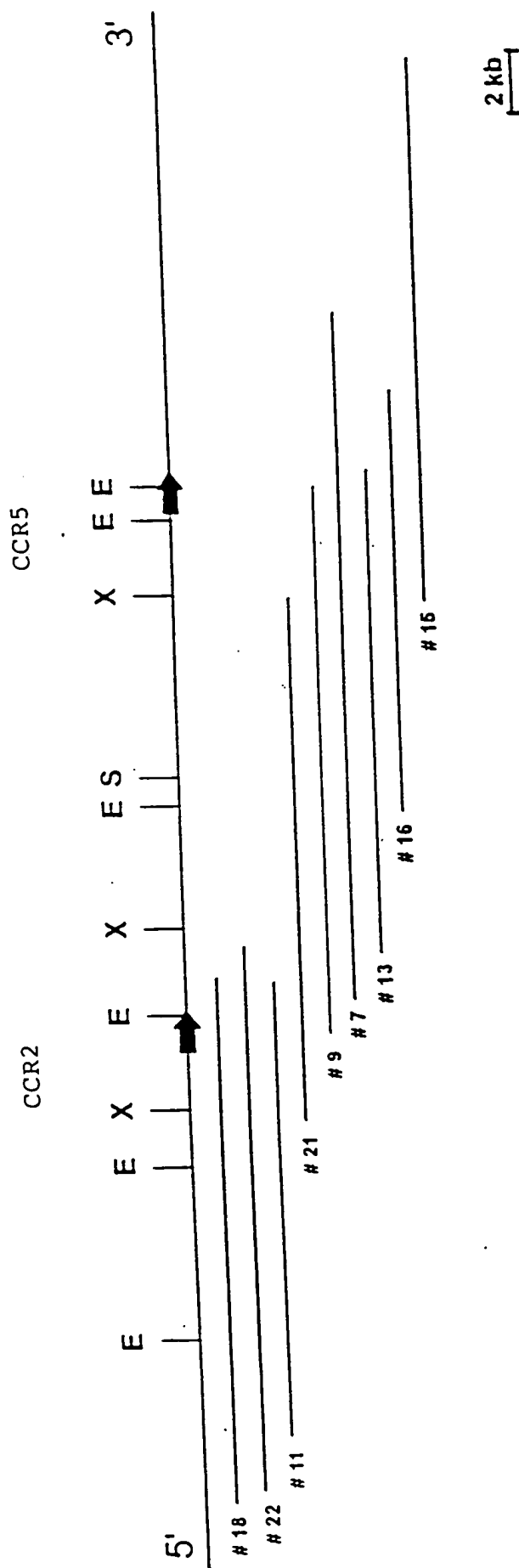
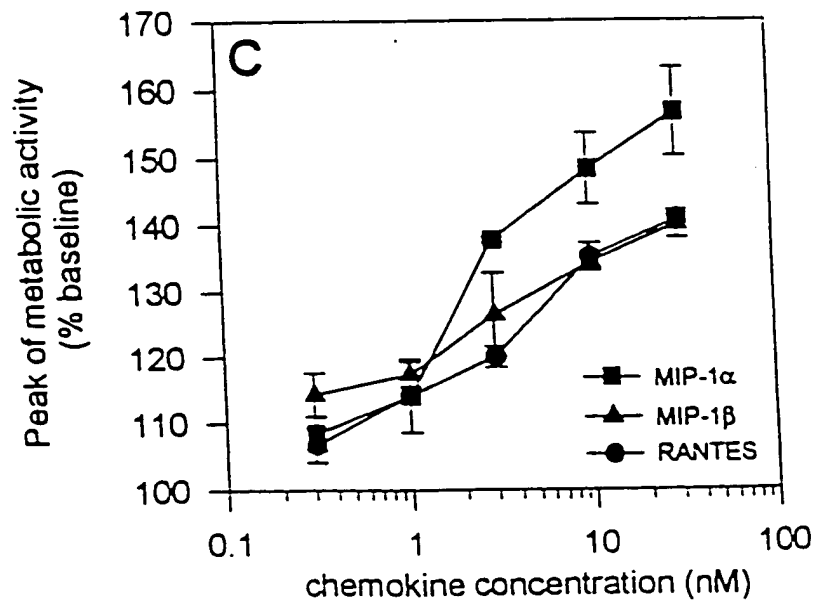
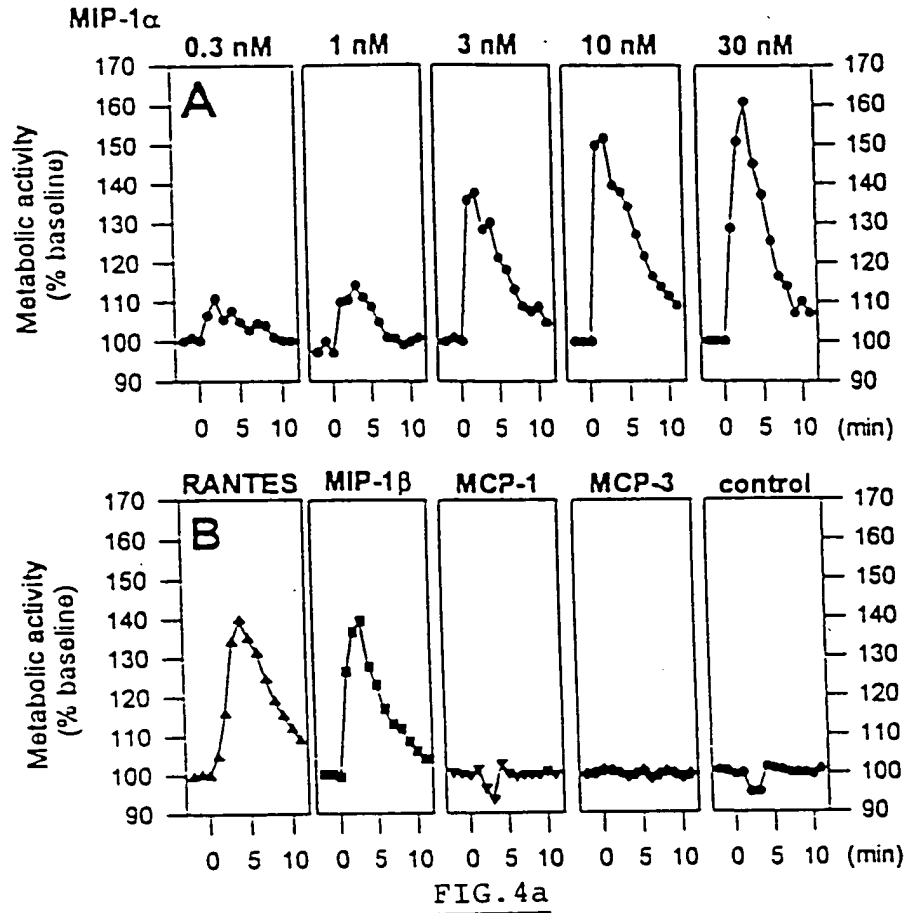


FIG. 3

**FIG. 4b**

104280" 92262660

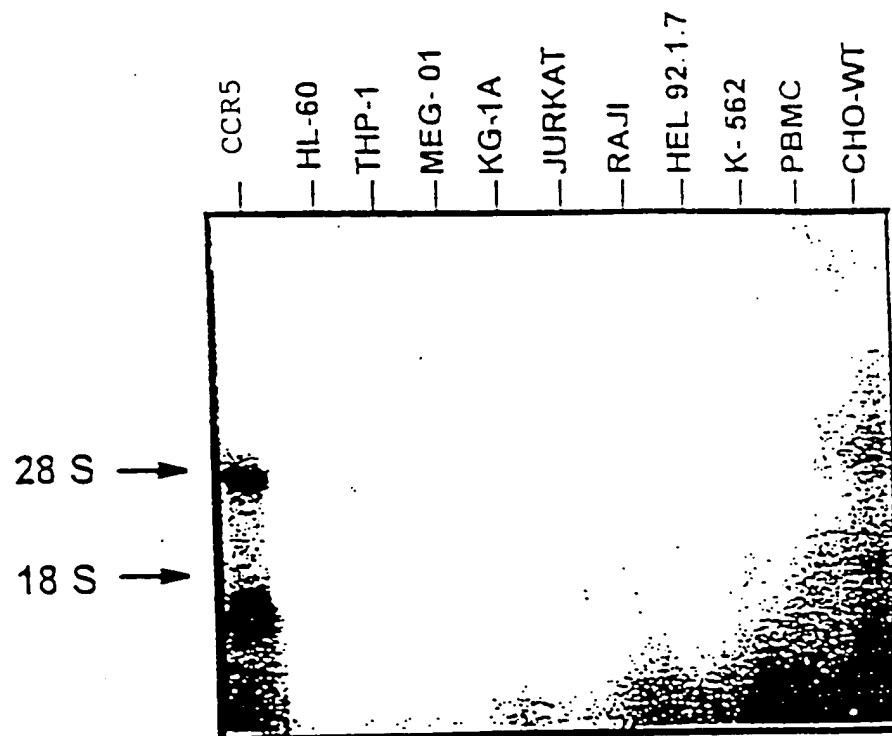
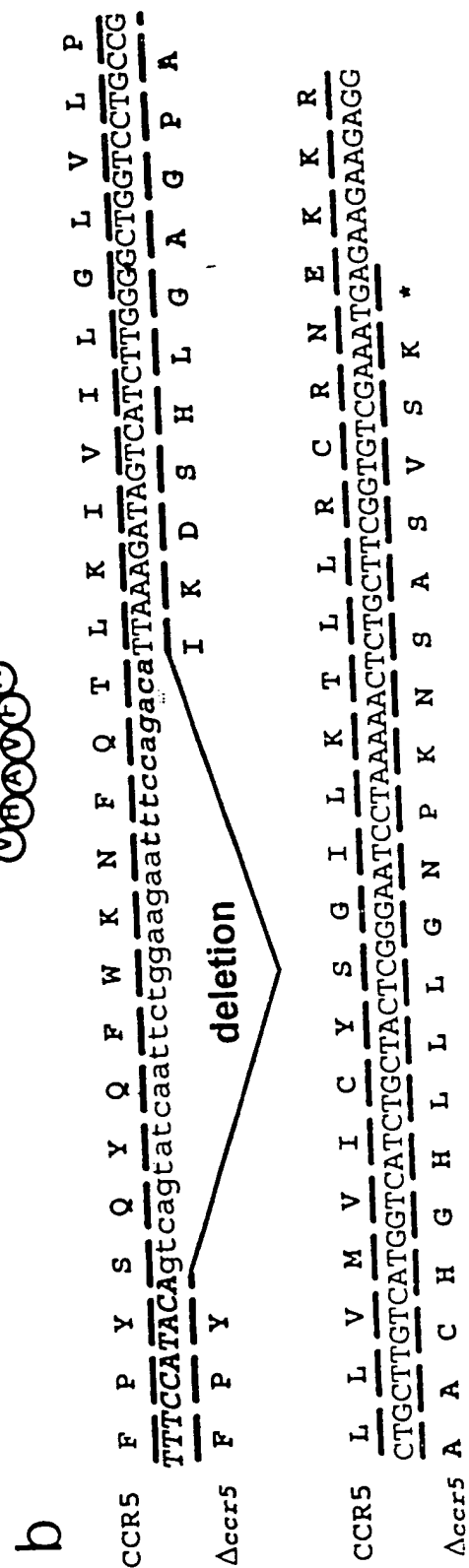
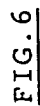


FIG. 5



A.

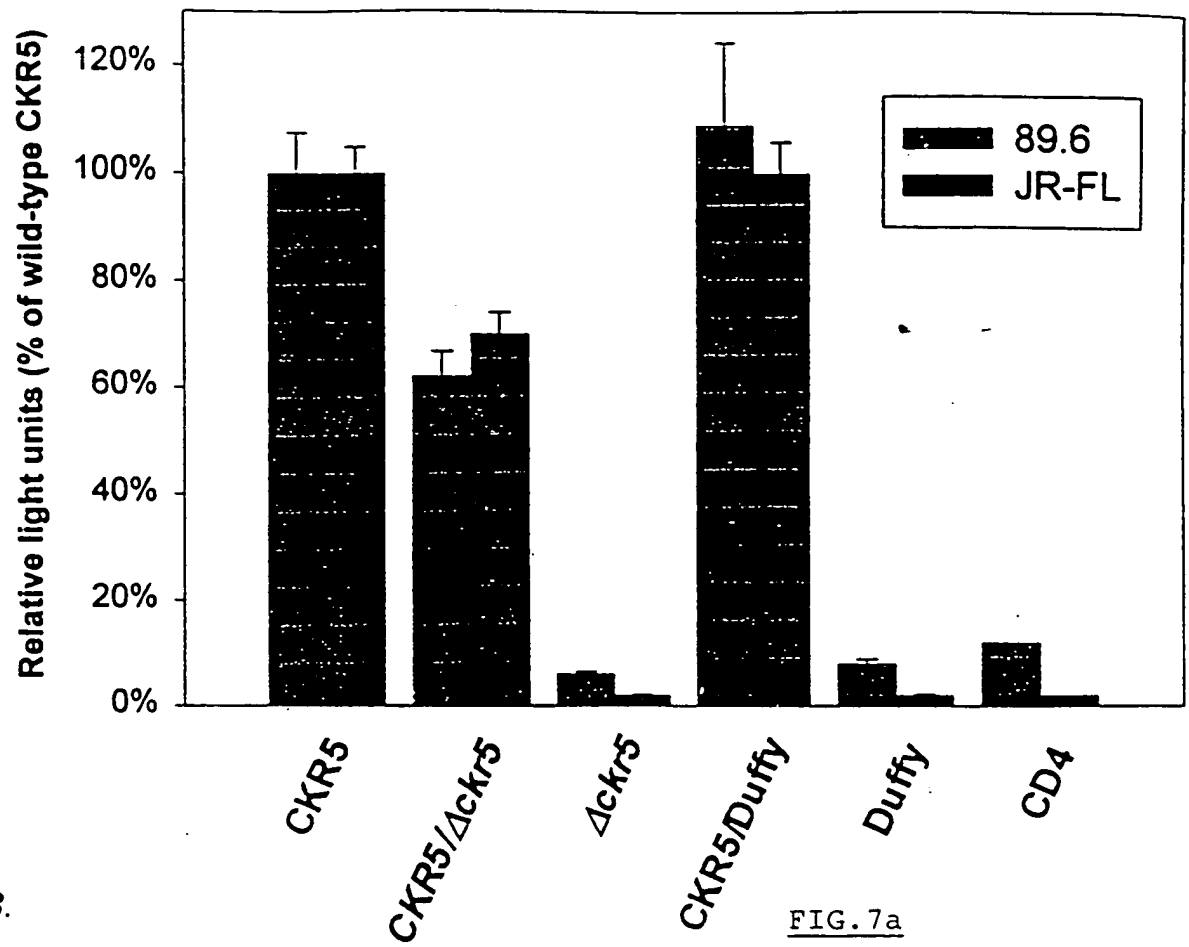


FIG. 7a

B.

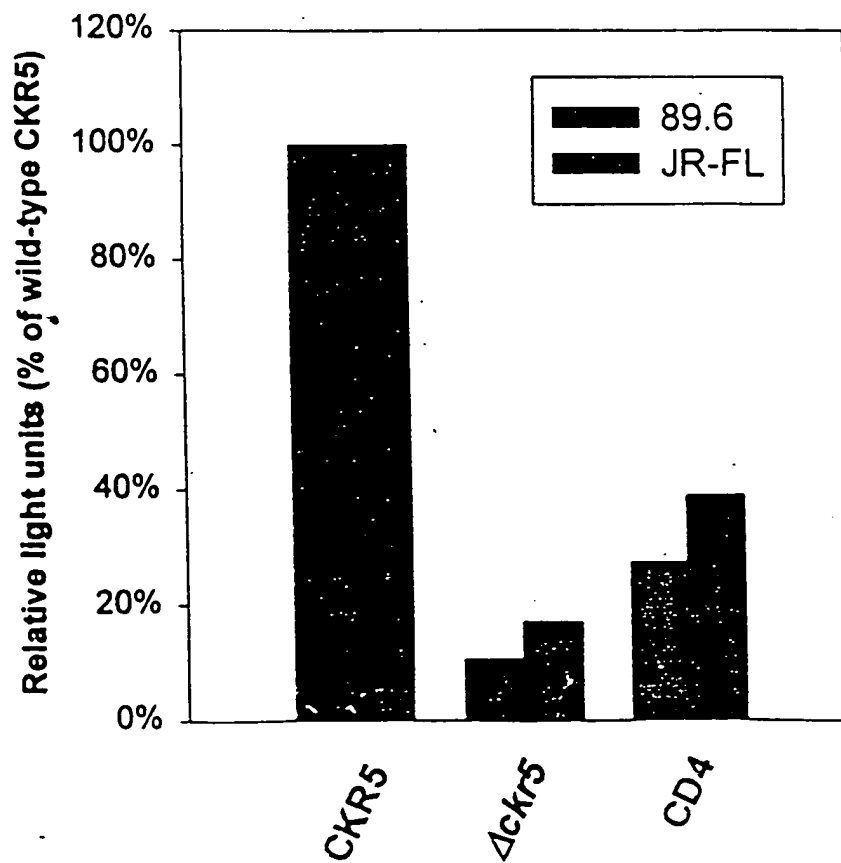


FIG. 7b

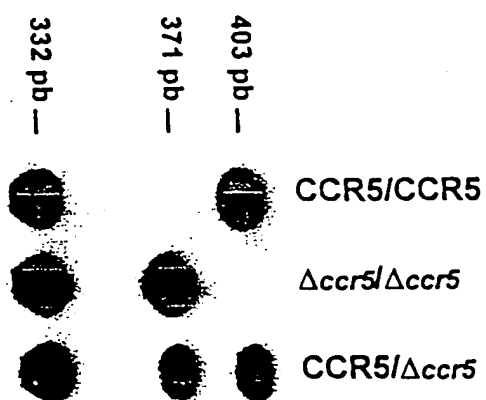


FIG.8

09939226.08240.1

FOI280" 9226E660

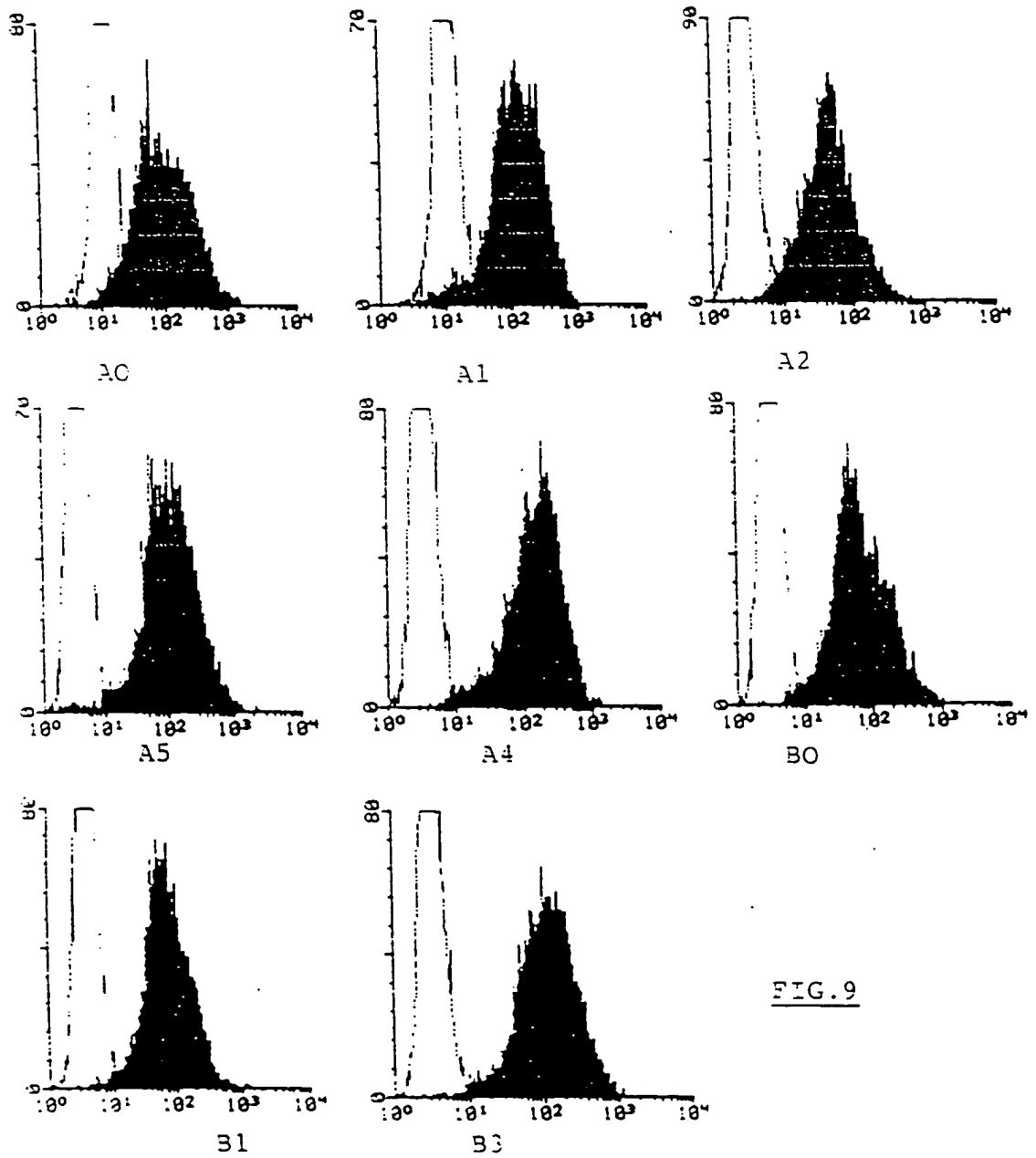


FIG. 9

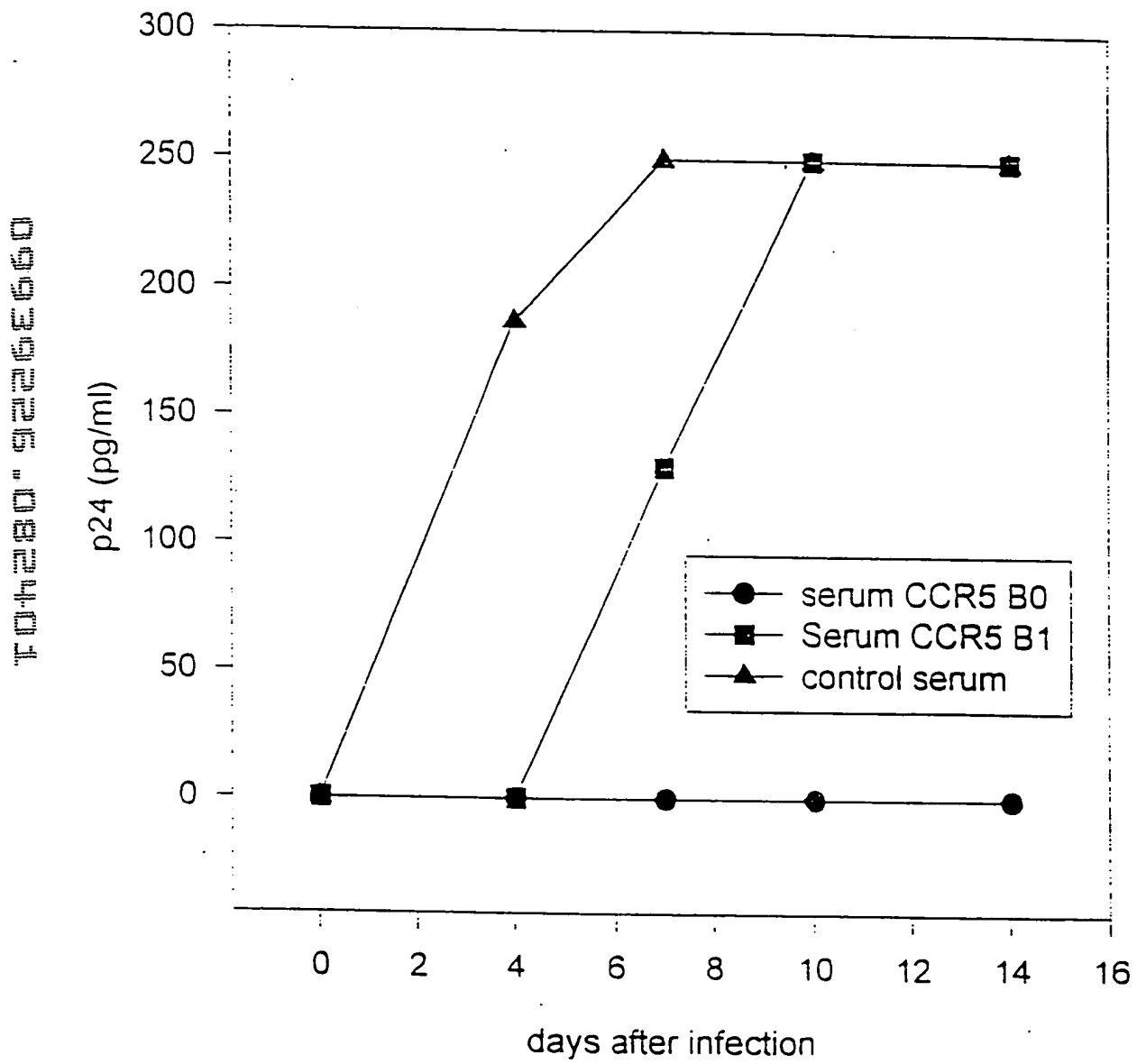


FIG.10